

SEQUENCE LISTING

<110> Glucksmann, Maria Aleksandra
Gimeno, Ruth
White, David

<120> 57242, a Human G-Protein Coupled
Receptor Family Member and Uses Therefor

<130> MPI2000-368P1R

<150> US 60/228,409

<151> 2000-08-29

<160> 9

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1194

<212> DNA

<213> human

<220>

<221> CDS

<222> (154)...(1194)

```

<400> 1
gcaccagcca acccacacac acaggaccgc catctgggt gatgaagtca gacacrcagc 60
agctgggtga gtgctaaccg tcagataagc atctgtgccca ttgtggggac tccctgggct 120
gctctgcacc cggacacctg ctctgtcccc gcc atg tac aac ggg tcg tgc tgc 174
               Met Tyr Asn Gly Ser Cys Cys
               1               5

cgc atc gag ggg gac acc atc tcc cag gtg atg ccg ccg ctg ctc att 222
Arg Ile Glu Gly Asp Thr Ile Ser Gln Val Met Pro Pro Leu Leu Ile
               10               15

gtg gcc ttt gtg ctg ggc gca cta ggc aat ggg gtc gcc ctg tgt ggt 270
Val Ala Phe Val Leu Gly Ala Leu Gly Asn Gly Val Ala Leu Cys Gly
               25               30

ttc tgc ttc cac atg aag acc tgg aag ccc agc act gtt tac ctt ttc 318
Phe Cys Phe His Met Lys Thr Trp Lys Pro Ser Thr Val Tyr Leu Phe
               40               45               50               55

aat ttg gcc gtg gct gat ttc ctc ctt atg atc tgc ctg cct ttt cgg 366
Asn Leu Ala Val Ala Asp Phe Leu Leu Met Ile Cys Leu Pro Phe Arg
               60               65               70

aca gac tat tac ctc aga cgt aga cac tgg gct ttt ggg gac att ccc 414
Thr Asp Tyr Tyr Leu Arg Arg Arg His Trp Ala Phe Gly Asp Ile Pro
               75               80               85

tgc cga gtg ggg ctc ttc acg ttg gcc atg aac agg gcc ggg agc atc 462
Cys Arg Val Gly Leu Phe Thr Leu Ala Met Asn Arg Ala Gly Ser Ile
               90               95               100

gtg ttc ctt acg gtg gtg gct gcg gac agg tat ttc aaa gtg gtc cac 510
Val Phe Leu Thr Val Val Ala Ala Asp Arg Tyr Phe Lys Val Val His
               105               110               115

ccc cac cac gcg gtg aac act atc tcc acc cgg gtg gcg gct ggc atc 558
Pro His His Ala Val Asn Thr Ile Ser Thr Arg Val Ala Ala Gly Ile
               120               125               130               135

gtc tgc acc ctg tgg gcc ctg gtc atc ctg gga aca gtg tat ctt ttg 606

```

Val	Cys	Thr	Leu	Trp	Ala	Leu	Val	Ile	Leu	Gly	Thr	Val	Tyr	Leu	Leu		
				140					145					150			
ctg	gag	aac	cat	ctc	tgc	gtg	caa	gag	acg	gcc	gtc	tcc	tgt	gag	agc	654	
Leu	Glu	Asn	His	Leu	Cys	Val	Gln	Glu	Thr	Ala	Val	Ser	Cys	Glu	Ser		
			155					160					165				
ttc	atc	atg	gag	tgc	gcc	aat	ggc	tgg	cac	gac	atc	atg	ttc	cag	ctg	702	
Phe	Ile	Met	Glu	Ser	Ala	Asn	Gly	Trp	His	Asp	Ile	Met	Phe	Gln	Leu		
			170				175					180					
gag	ttc	ttt	atg	ccc	ctc	ggc	atc	atc	tta	ttt	tgc	tcc	ttc	aag	att	750	
Glu	Phe	Phe	Met	Pro	Leu	Gly	Ile	Ile	Leu	Phe	Cys	Ser	Phe	Lys	Ile		
			185			190					195						
gtt	tgg	agc	ctg	agg	cgg	agg	cag	cag	ctg	gcc	aga	cag	gct	cgg	atg	798	
Val	Trp	Ser	Leu	Arg	Arg	Gln	Gln	Leu	Ala	Arg	Gln	Ala	Arg	Met			
					205					210				215			
aag	aag	gcg	acc	cgg	ttc	atc	atg	gtg	gtg	gca	att	gtg	ttc	atc	aca	846	
Lys	Lys	Ala	Thr	Arg	Phe	Ile	Met	Val	Val	Ala	Ile	Val	Phe	Ile	Thr		
				220						225				230			
tgc	tac	ctg	ccc	agc	gtg	tct	gct	aga	ctc	tat	ttc	ctc	tgg	acg	gtg	894	
Cys	Tyr	Leu	Pro	Ser	Val	Ser	Ala	Arg	Leu	Tyr	Phe	Leu	Trp	Thr	Val		
				235				240					245				
ccc	tgc	agt	gcc	tgc	gat	ccc	tct	gtc	cat	ggg	gcc	ctg	cac	ata	acc	942	
Pro	Ser	Ser	Ala	Cys	Asp	Pro	Ser	Val	His	Gly	Ala	Leu	His	Ile	Thr		
				250			255					260					
ctc	agc	ttc	acc	tac	atg	aac	agc	atg	ctg	gat	ccc	ctg	gtg	tat	tat	990	
Leu	Ser	Phe	Thr	Tyr	Met	Asn	Ser	Met	Leu	Asp	Pro	Leu	Val	Tyr	Tyr		
						270					275						
ttt	tca	agc	ccc	tcc	ttt	ccc	aaa	ttc	tac	aac	aag	ctc	aaa	atc	tgc	1038	
Phe	Ser	Ser	Pro	Ser	Phe	Pro	Lys	Phe	Tyr	Asn	Lys	Leu	Lys	Ile	Cys		
						285				290				295			
agt	ctg	aaa	ccc	aag	cag	cca	gga	cac	tca	aaa	aca	caa	agg	ccg	gaa	1086	
Ser	Leu	Lys	Pro	Lys	Gln	Pro	Gly	His	Ser	Lys	Thr	Gln	Arg	Pro	Glu		
						300			305					310			
gag	atg	cca	att	tgc	aac	ctc	ggt	cgc	agg	agt	tgc	atc	agt	gtg	gca	1134	
Glu	Met	Pro	Ile	Ser	Asn	Leu	Gly	Arg	Arg	Ser	Cys	Ile	Ser	Val	Ala		
						315			320				325				
aat	agt	ttc	caa	agc	cag	tct	gat	ggg	caa	tgg	gat	ccc	cac	att	gtt	1182	
Asn	Ser	Phe	Gln	Ser	Gln	Ser	Asp	Gly	Gln	Trp	Asp	Pro	His	Ile	Val		
						330		335				340					
gag	tgg	cac	tga													1194	
Glu	Trp	His	*														
				345													

<210> 2
 <211> 346
 <212> PRT
 <213> human

<400> 2
 Met Tyr Asn Gly Ser Cys Cys Arg Ile Glu Gly Asp Thr Ile Ser Gln
 1 5 10 15
 Val Met Pro Pro Leu Leu Ile Val Ala Phe Val Leu Gly Ala Leu Gly
 20 25 30
 Asn Gly Val Ala Leu Cys Gly Phe Cys Phe His Met Lys Thr Trp Lys
 35 40 45
 Pro Ser Thr Val Tyr Leu Phe Asn Leu Ala Val Ala Asp Phe Leu Leu

50	Met	Ile	Cys	Leu	Pro	Phe	Arg	Thr	Asp	Tyr	Tyr	55	Leu	Arg	Arg	Arg	His
65	Trp	Ala	Phe	Gly	Asp	Ile	Pro	Cys	Arg	Val	Gly	70	Leu	Phe	Thr	Leu	Ala
				85						90						95	
	Met	Asn	Arg	Ala	Gly	Ser	Ile	Val	Phe	Leu	Thr	100	Val	Val	Ala	Ala	Asp
				100								105				110	
	Arg	Tyr	Phe	Lys	Val	Val	His	Pro	His	His	Ala	115	Val	Asn	Thr	Ile	Ser
				115								120				125	
	Thr	Arg	Val	Ala	Ala	Gly	Ile	Val	Cys	Thr	Leu	130	Trp	Ala	Leu	Val	Ile
							135					140					
	Leu	Gly	Thr	Val	Tyr	Leu	Leu	Glu	Asn	His	Leu	145	Cys	Val	Gln	Glu	
							150					155				160	
	Thr	Ala	Val	Ser	Cys	Glu	Ser	Phe	Ile	Met	Glu	170	Ser	Ala	Asn	Gly	Trp
							165					175					
	His	Asp	Ile	Met	Phe	Gln	Leu	Glu	Phe	Phe	Met	180	Pro	Leu	Gly	Ile	Ile
							185					190					
	Leu	Phe	Cys	Ser	Phe	Lys	Ile	Val	Trp	Ser	Leu	200	Arg	Arg	Arg	Gln	Gln
							205					210					
	Leu	Ala	Arg	Gln	Ala	Arg	Met	Lys	Lys	Ala	Thr	215	Phe	Ile	Met	Val	
							220					225					
	Val	Ala	Ile	Val	Phe	Ile	Thr	Cys	Tyr	Leu	Pro	230	Ser	Val	Ser	Ala	Arg
							235					240					
	Leu	Tyr	Phe	Leu	Trp	Thr	Val	Pro	Ser	Ser	Ala	245	Cys	Asp	Pro	Ser	Val
							250					255					
	His	Gly	Ala	Leu	His	Ile	Thr	Leu	Ser	Phe	Thr	260	Tyr	Met	Asn	Ser	Met
							265					270					
	Leu	Asp	Pro	Leu	Val	Tyr	Tyr	Phe	Ser	Ser	Pro	275	Ser	Phe	Pro	Lys	Phe
							280					285					
	Tyr	Asn	Lys	Leu	Lys	Ile	Cys	Ser	Leu	Lys	Pro	290	Lys	Gln	Pro	Gly	His
							295					300					
	Ser	Lys	Thr	Gln	Arg	Pro	Glu	Glu	Met	Pro	Ile	305	Ser	Asn	Leu	Gly	Arg
							310					315					
	Arg	Ser	Cys	Ile	Ser	Val	Ala	Asn	Ser	Phe	Gln	320	Ser	Gln	Ser	Asp	Gly
							325					330					
	Gln	Trp	Asp	Pro	His	Ile	Val	Glu	Trp	His		335					
							340					345					

<210> 3
 <211> 1041
 <212> DNA
 <213> human

<400> 3
 atgtacaacg ggtcgtgctg cgcgcacgag ggggacacca tctcccagggt gatgccgcg 60
 ctgctcaattg tggccttttgt gctggggcga ctaggcaatg ggggtcgccct gtgtggtttc 120
 tgccttcaca tgaagacctg gaagcccagc actgtttacc ttccaattt ggccgtggct 180
 gatttctctc ttatgatctg cctgcctttt cggacagact attaccctag acgtagacac 240
 tgggcttttg gggacattcc ctgccgagtg gggctcttca cgttggccat gaacaggccc 300
 gggagatcgt tggctctttac ggtggtggct gcggacaggt atttcaaagt ggtccacccc 360
 caccacgcgt tgaacactat ctccaccggg gtggcgctgt caccctgtgg 420
 gccctggcta tctctgggaac agtgtatctt ttgctggaga accatctctg cgtgcaagag 480
 accggcgctct cctgtgagag ctctcatcat gactcgccga atggctggca cgacatcatg 540
 ttccagctgg agttctttat gccctctggc atcatcttat ttgtctctt caagatttgt 600
 tggagcctga ggcggaggca gcagctggcc agacaggctc ggatgaagaa ggcgaccggc 660
 ttcatcatgg tgggtggaat tgtgttcatc acatgctacc tgcccagcgt gtctgctaga 720
 ctctattttc tctggacggt gccctcgagt gcctgcgata cctctgtoca tggggccctg 780
 cacataacc tcagcttctac ctacatgaac agcatgctgg atcccctggt gtattatttt 840
 tcaaacccct cttttcccaa attctacaac aagctcaaaa tctgcagctc gaacccaag 900
 cagccaggac actcaaaaac acaaaggccg gaagagatgc caatttcgaa cctcggtcgc 960
 aggaattgca tcaagtgtgc aaatatgttc caaagccagt ctgatgggca atgggattcc 1020
 cacattgttg agtggcactg a

<210> 4
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> murine 57242 primer sequence
 <400> 4 19
 ggcagcagct gaccagaca
 <210> 5
 <211> 21
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> murine 57242 primer sequence
 <400> 5 21
 gaacacagaa gccaccacca t
 <210> 6
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> murine 57242 probe sequence
 <400> 6 23
 atgaggaggg ccacccggtt cat
 <210> 7
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> human 57242 primer sequence
 <400> 7 20
 tgcagtctga aaccaagca
 <210> 8
 <211> 17
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> human 57242 primer sequence
 <400> 8 17
 tgcgaccgag gttcgaa
 <210> 9
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> human 57242 probe sequence
 <400> 9 23
 cacaaaggcc ggaagagatg cca